Fig. 1A

METOTP-1.SEQ4 -> Restriction Map

DNA sequence 540 b.p. ATGTGGTACCAG … CCGTAAGGTACC linear

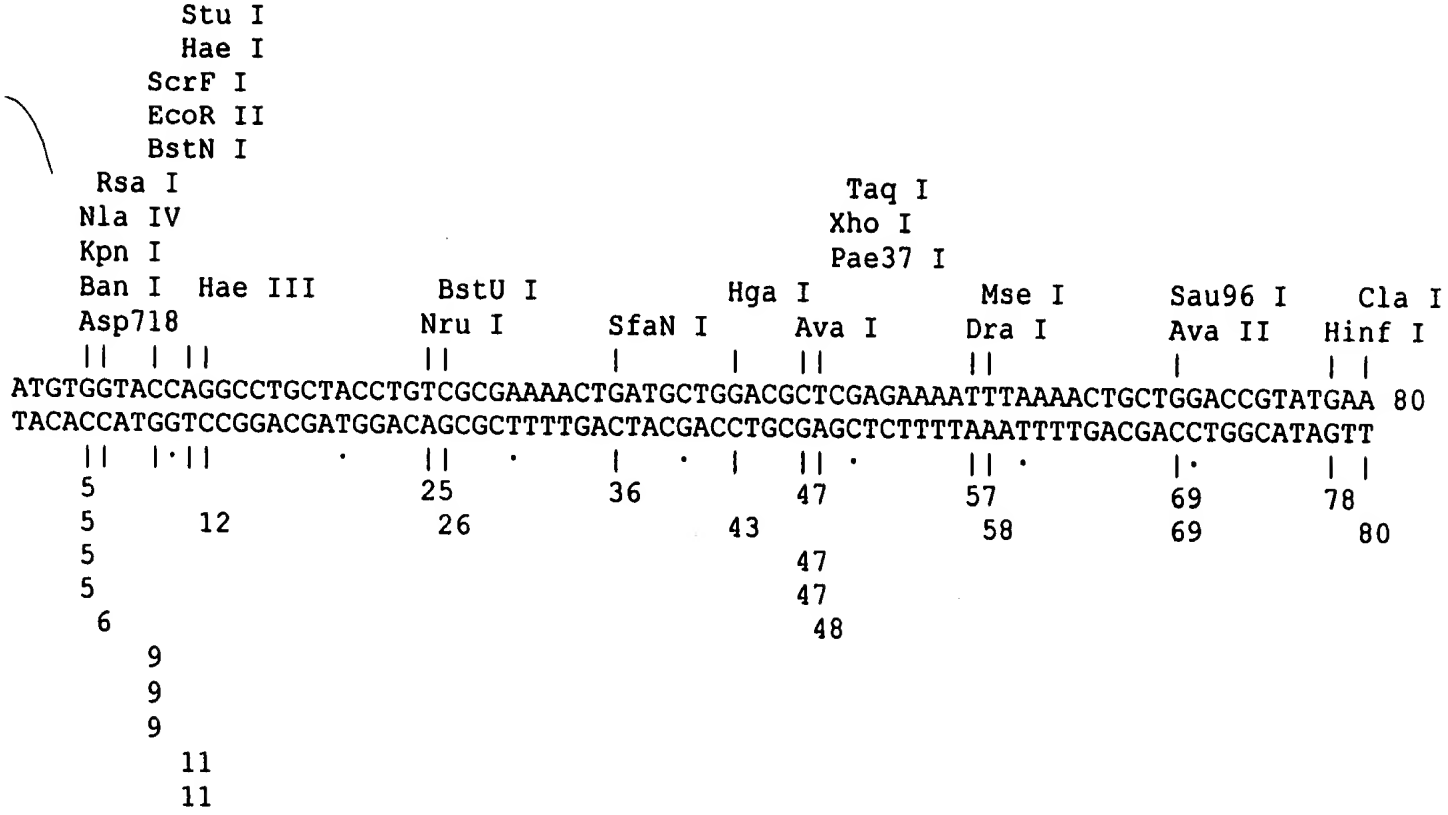


Fig. 1B

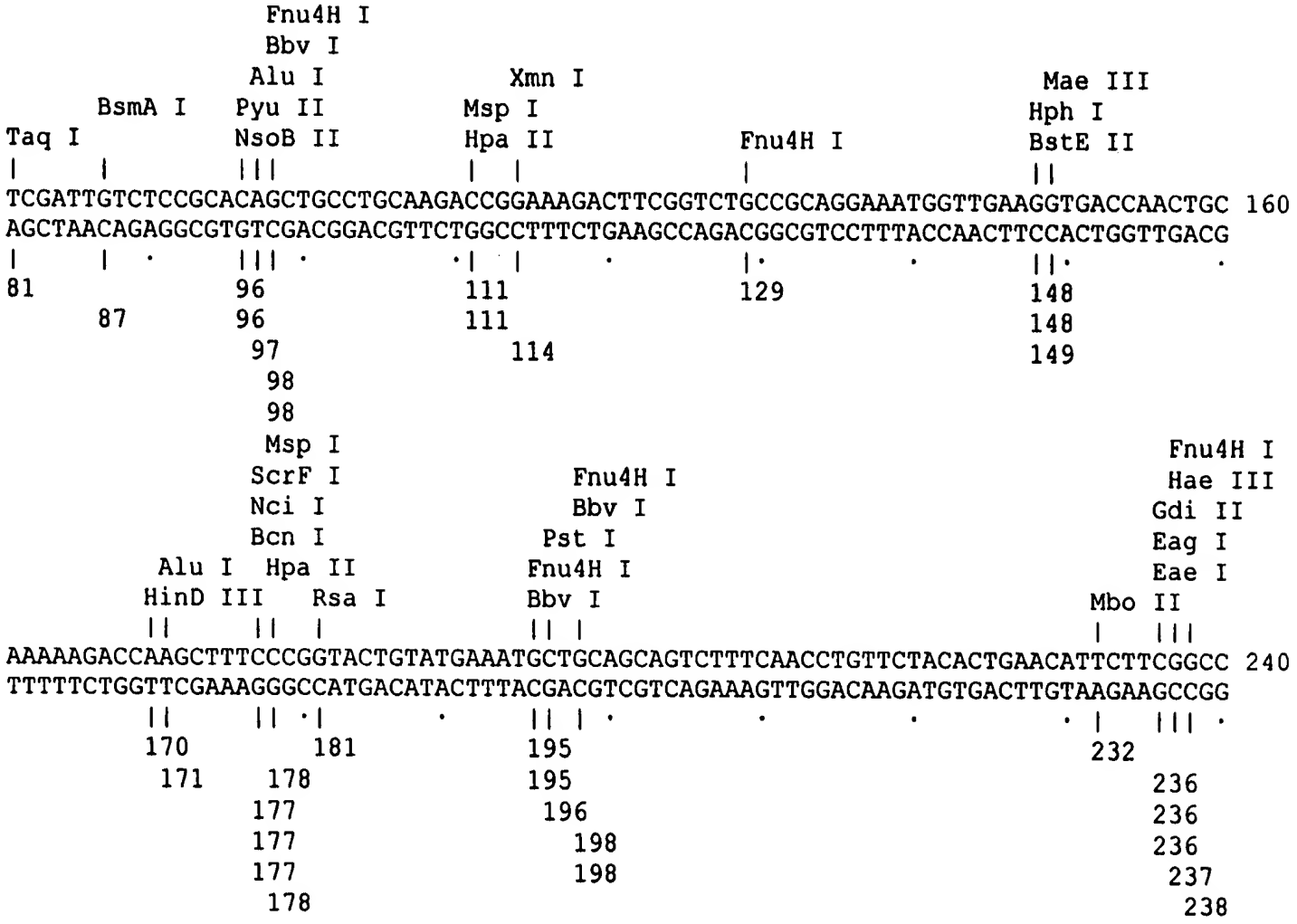


Fig. 1C

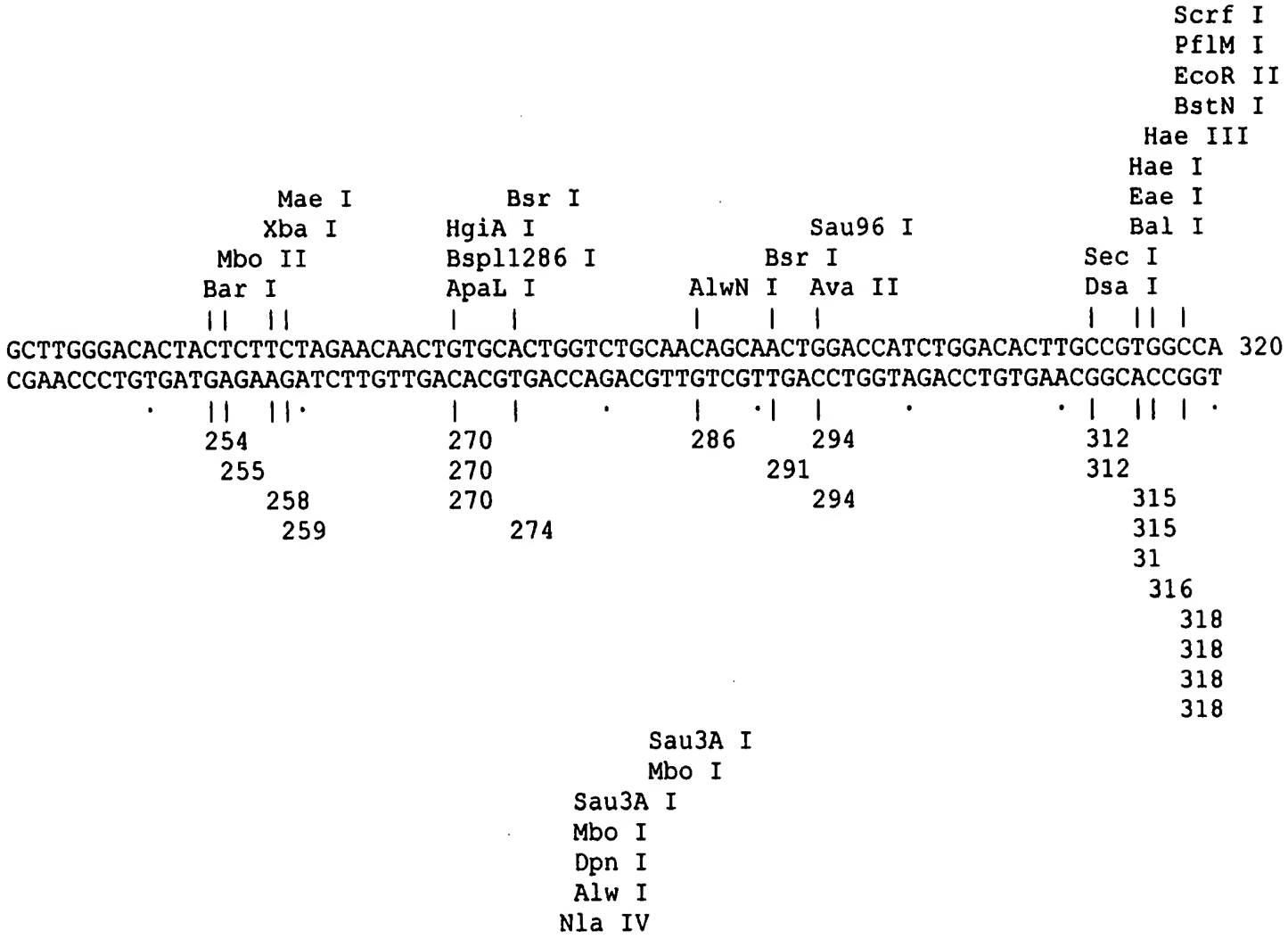

Scrf I
PflM I
EcoR II
BstN I
Hae III
Hae I
Eae I
Bal I
Sec I
Dsa I
Mae I
Xba I
Mbo II
Bar I
Bsr I
HgiA I
Bspl1286 I
ApaL I
Sau96 I
Bsr I
AlwN I
Ava II
GCTTGGGACACTACTCTTCTAGAACAACTGTGCACTGGTCTGCAACAGCAACTGGACCATCTGGACACTTGCCGTGGCCA 320
CGAACCCTGTGATGAGAAGATCTTGTTGACACGTGACCAGACGTTGTCGTTGACCTGGTAGACCTGTGAACGGCACCGGT
254
255
258
259
270
270
270
274
286
291
294
294
312
312
315
315
31
316
318
318
318
318
Sau3A I
Mbo I
Sau3A I
Mbo I
Dpn I
Alw I
Nla IV

Fig. 1D

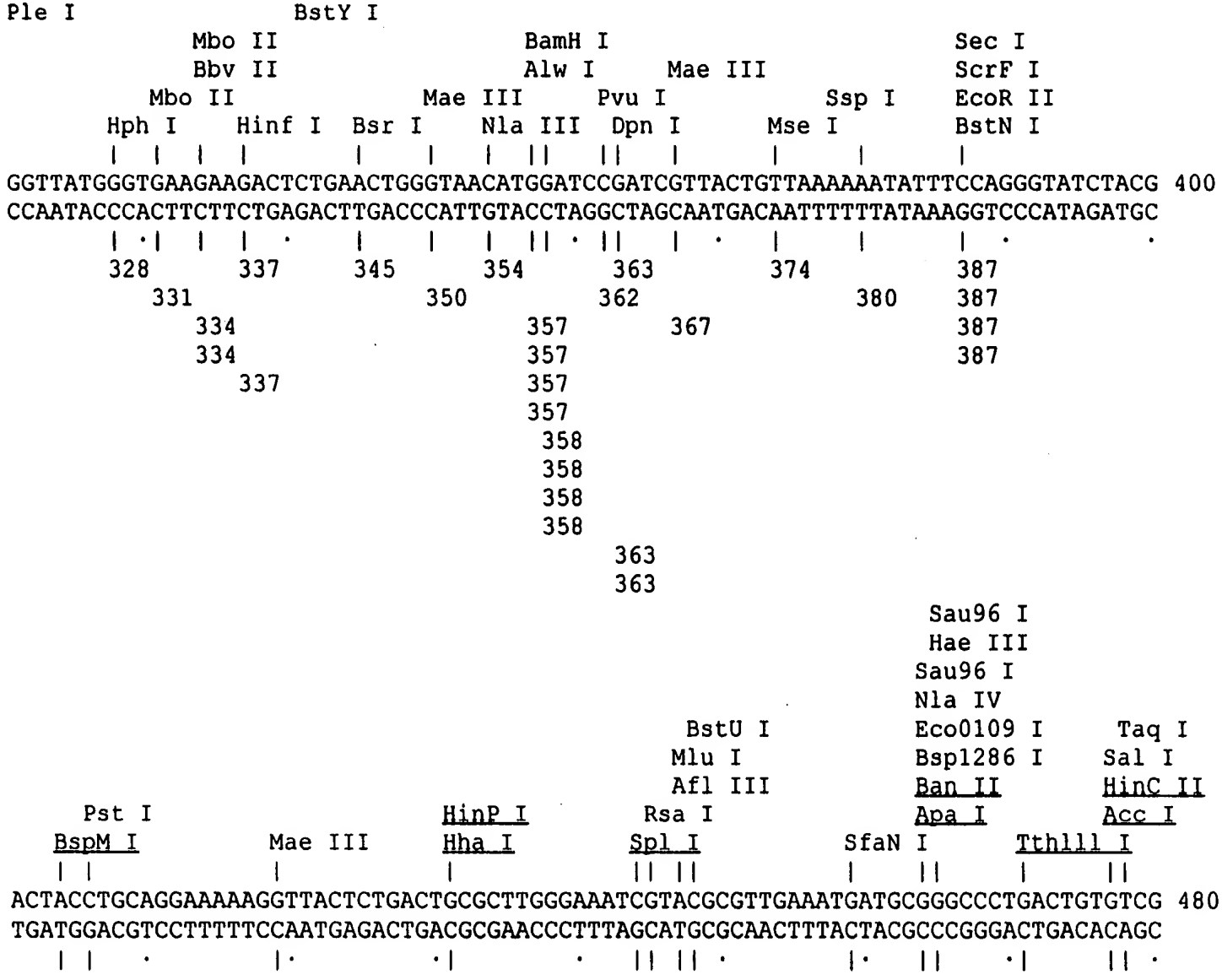
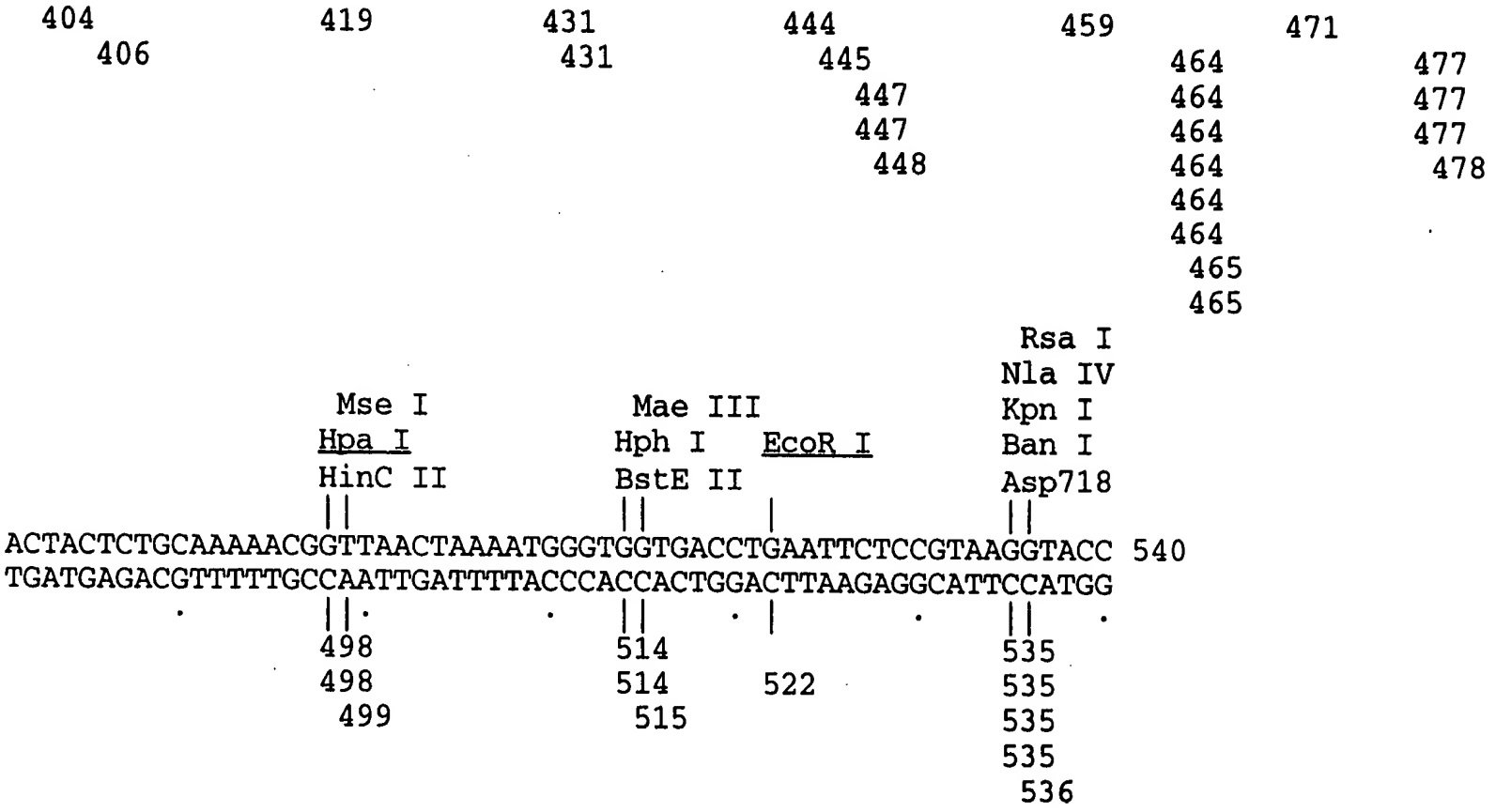


Fig. 1E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477
477
477
478
Rsa I
Nla IV
Kpn I
Ban I
Asp718
Mse I
Hpa I
HinC II
Mae III
Hph I
BstE II
EcoR I
ACTACTCTGCAAAAACGGTTAACTAAAATGGGTGGTGACCTGAATTCTCCGTAAGGTACC 540
TGATGAGACGTTTTTGCCAATTGATTTTACCCACCACTGGACTTAAGAGGCATTCCATGG
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514
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535
536

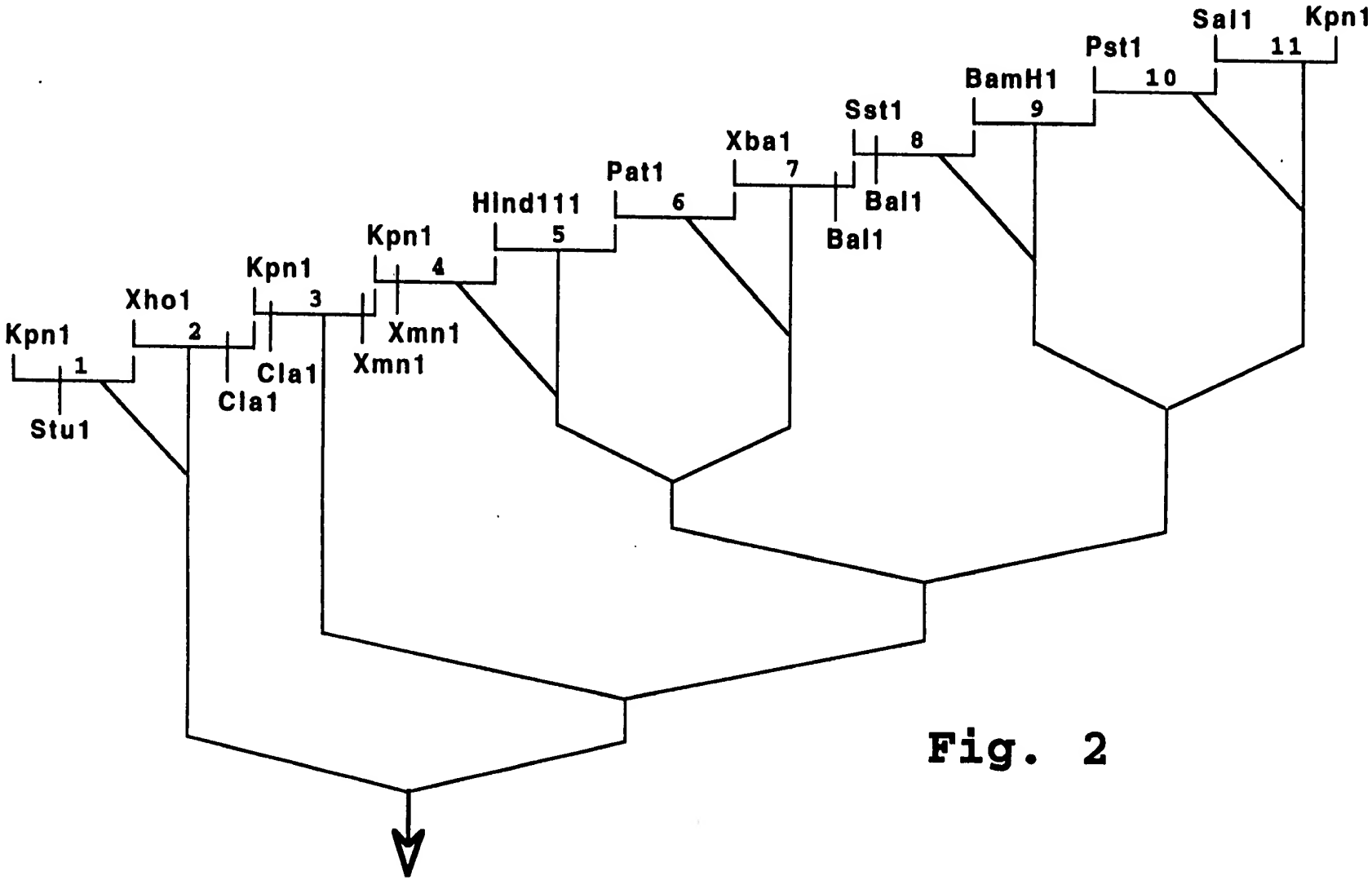

Kpn1
1
Stu1
Xho1
2
Cla1
Cla1
Kpn1
3
Kpn1
4
Xmn1
Xmn1
Hind111
5
Pat1
6
Xba1
7
Sst1
8
Bal1
Bal1
BamH1
9
Pst1
10
Sal1
11
Kpn1

Fig. 2

```
                    -23                                                  -9
                    met ala phe val leu ser leu leu met ala leu val leu val ser
oIFNτ       cccc ATG GCC TTC GTG CTC TCT CTA CTG ATG GCC CTG GTG CTG GTC AGC
htIFN       cccc ATG GCC TTC GTG CTC TCT CTA CTC ATG GCC CTG GTG CTG GTC AGC

-8                                 -1  +1                                11
tyr gly pro gly gly ser leu gly cys tyr leu ser arg lys leu met leu asp ala
TAT GGC CCA GGA GGA TCT CTG GGT TGT TAC CTA TCT CGG AAA CTC ATG CTG GAT GCC
TAC GGC CCA GGA GGA TCC CTG GGT TGT GAC CTG TCT CAG AAC CAC GTG CTG GTT GGC

 12                                 20                                  30
arg glu asn leu lys leu leu asp arg met asn arg leu ser pro his ser cys leu
AGG GAG AAC CTC AAG CTC CTG GAC CGA ATG AAC AGA CTC TCC CCT CAT TCC TGT CTG
AGG AAG AAC CTC AGG CTC CTG GAC GAA ATG AGG AGA CTC TCC CCT CGC TTT TGT CTG

31                                 40                                  49
gln asp arg lys asp phe gly leu pro gln glu met val glu gly asp gln leu gln
CAG GAC AGA AAA GAC TTT GGT CTT CCC CAG GAG ATG GTG GAG GGC GAC CAG CTC CAG
CAG GAC AGA AAA GAC TTC GCT TTA CCC CAG GAA ATG GTG GAG GGC GGC CAG CTC CAG

50                                 60                                  68
lys asp gln ala phe pro val leu tyr glu met leu gln gln ser phe asn leu phe
AAG GAC CAG GCC TTC CCT GTG CTC TAC GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC
GAG GCC CAG GCC ATC TCT GTG CTC CAT GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC

69   70                                 80                                  87
tyr thr glu his ser ser ala ala try asp thr thr leu leu glu gln leu cys thr
TAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC CTC CTG GAG CAG CTC TGC ACT
CAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC CTC CTG GAG CAG CTC CGC ACT

88       90                                100                         106
gly leu gln gln gln leu asp his leu asp thr cys arg gly gln val met gly glu
GGA CTC CAA CAG CAG CTG GAC CAC CTG GAC ACC TGC AGG GGT CAA GTG ATG GGA GAG
GGA CTC CAT CAG CAG CTG GAC AAC CTG GAT GCC TGC CTG GGG CAG GTG ATG GGA GAG

107         110                                120                 125
glu asp ser glu leu gly asn met asp pro ile val thr val lys lys tyr phe gln
GAA GAC TCT GAA CTG GGT AAC ATG GAC CCC ATT GTG ACC GTG AAG AAG TAC TTC CAG
GAA GAC TCT GCC CTG GGA AGG ACG GGC CCC ACC CTG GCT CTG AAG AGG TAC TTC CAG

126             130                                140             144
gly ile tyr asp tyr leu gln glu lys gly tyr ser asp cys ala trp glu ile val
GGC ATC TAT GAC TAC CTG CAA GAG AAG GGA TAC AGC GAC TGC GCC TGG GAA ATC GTC
GGC ATC CAT GTC TAC CTG AAA GAG AAG GGA TAC AGC GAC TGC GCC TGG GAA ACC GTC

145                 150                                160         163
arg val glu met met arg ala leu thr val ser thr thr leu gln lys arg leu thr
AGA GTC GAG ATG ATG AGA GCC CTC ACT GTA TCA ACC ACC TTG CAA AAA AGG TTA ACA
AGA CTG GAA ATC ATG AGA TCC TTC TCT TCA TTA ATC AGC TTG CAA GAA AGG TTA AGA

164                                172
lys met gly gly asp leu asn ser pro end
AAG ATG GGT GGA GAT CTG AAC TCA CCT TGA
ATG ATG GAT GGA GAC CTG AGC TCA CCT TGA
```

Fig. 3

Fig. 4

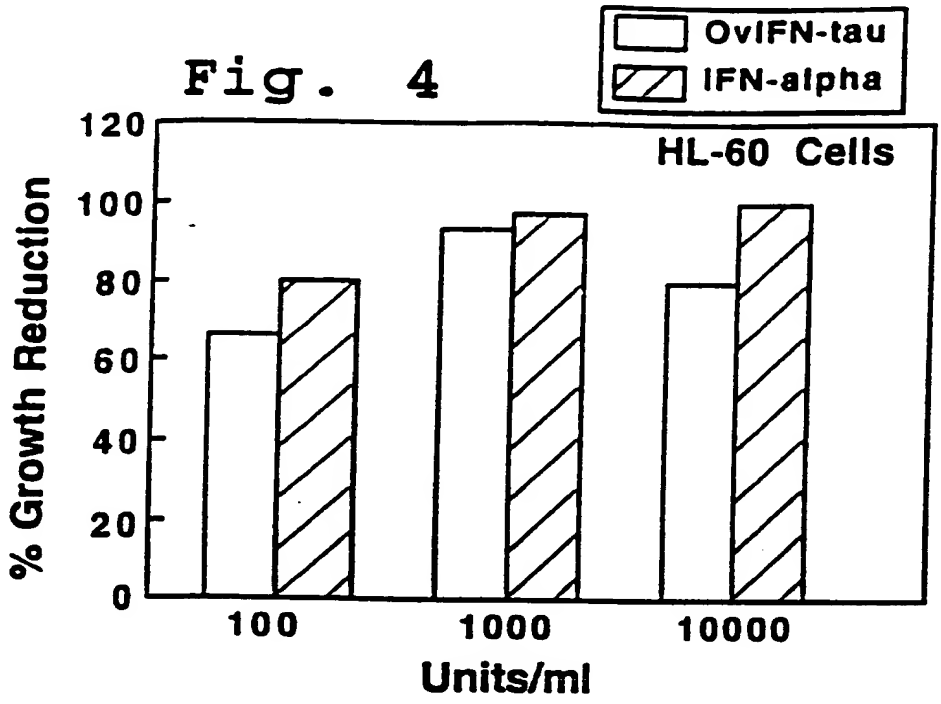
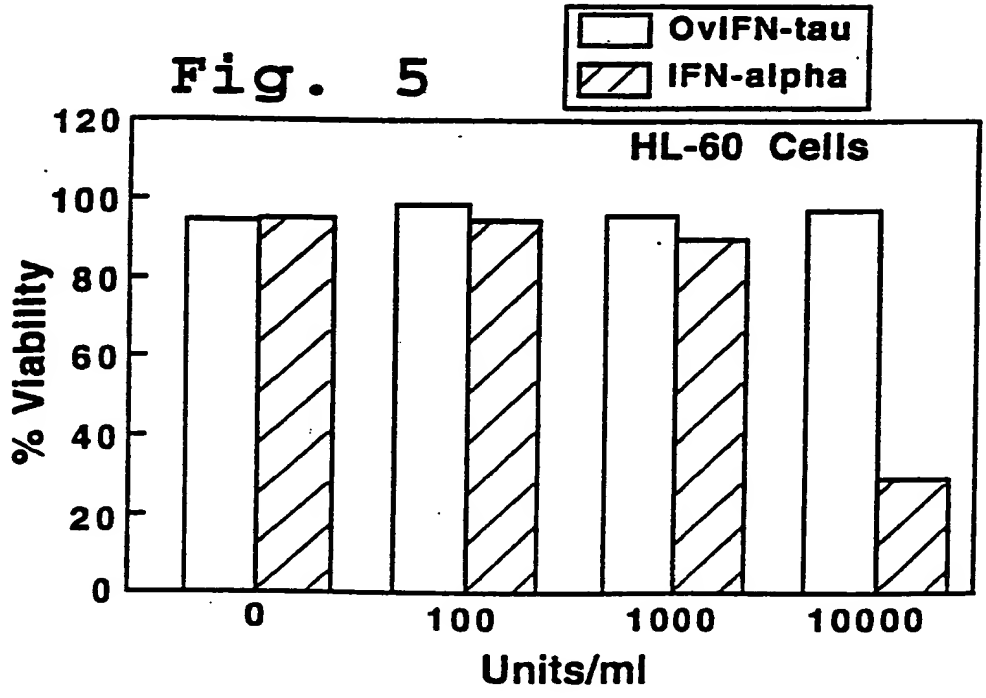


Fig. 5



Peptides	MW	HI*	Sequence
IFNt(1-37) (SEQ ID NO:5)	4465	-0.78	CYSLRKLMLDARENLKLLDRMNRLSPHSCLQDRKDFG
IFNt(34-64) (SEQ ID NO:6)	3610	-0.72	KDFGLPQEMVEGDQLQKDQAFPVLYEMLQQS
IFNt(62-92) (SEQ ID NO:7)	3586	-0.53	QQSFNLFYTEHSSAAWDTTLLEQLCTGLQQQ
IFNt(90-122) (SEQ ID NO:8)	3712	-0.86	QQQLDHLDTCRGQVMGEEDSELGNMDPIVTVKK
IFNt(119-150) (SEQ ID NO:9)	3948	-0.56	TVKKYFQGIYDYLQEKGYSDCAWEIVRVEMMR
IFNt(139-172) (SEQ ID NO:10)	3818	-0.11	CAWEIVRVEMMRALTVSTTLQKRLTKMGGDLNSP

*Hydropathic Index

Fig. 6

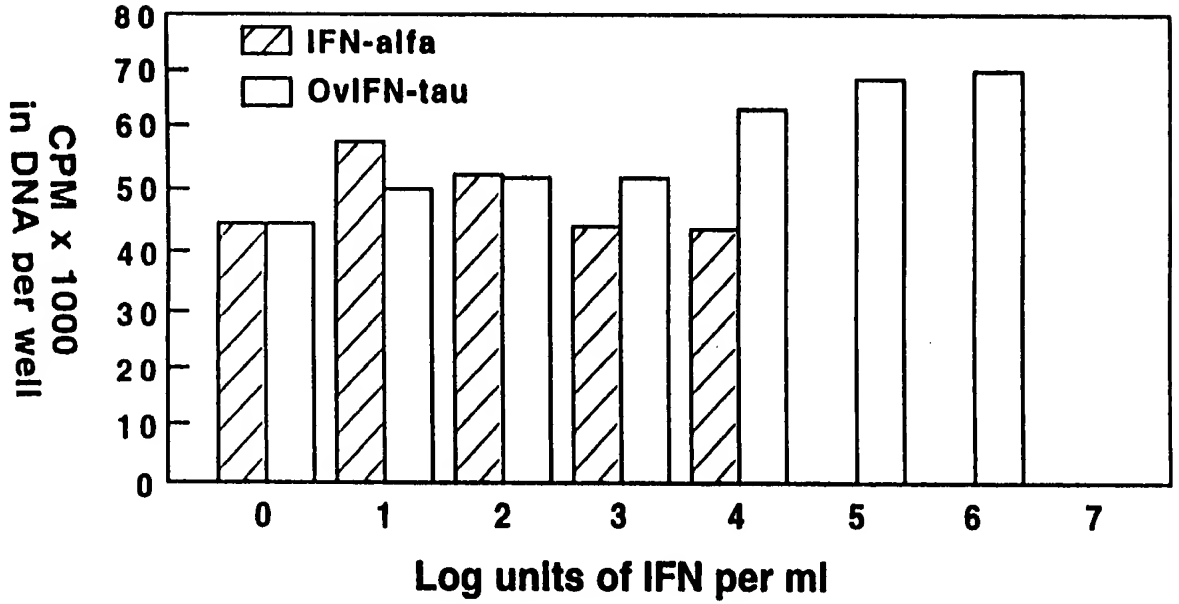
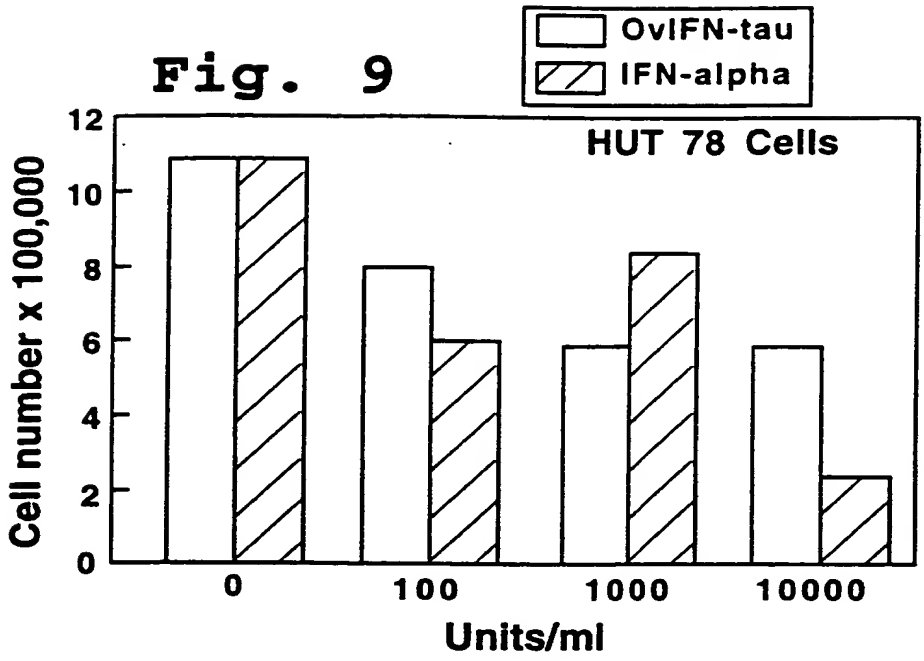


Fig. 8

```
1                                                                              80
CTGAGATGGGATCAGAGAACCTACCTGAAGGTTCCCCCTGACCCCATCTCAGCCAGCCCAGCAGCAGCCGCATCTTCCCC

 81                                                                          140
 ATG GCC TTC GTG CTC TCT CTA CTG ATG GCC CTG GTG CTG GTC AGC TAT GGC CCA GGA GGA
 S1                                                                          S20
 Met Ala Phe Val Leu Ser Leu Leu Met Ala Leu Val Leu Val Ser Tyr Gly Pro Gly Gly
141                                                                              200
 TCT CTG GGT TGT TAC CTA TCT CGG AAA CTC ATG CTG GAT GCC AGG GAG AAC CTC AAG CTC
 S21            ↓                                                             17
 Ser Leu Gly Cys Tyr Leu Ser Arg Lys Leu Met Leu Asp Ala Arg Glu Asn Leu Lys Leu
201                                                                              260
 CTG GAC CGA ATG AAC AGA CTC TCC CCT CAT TCC TGT CTG CAG GAC AGA AAA GAC TTT GGT
 18                                                                           37
 Leu Asp Arg Met Asn Arg Leu Ser Pro His Ser Cys Leu Gln Asp Arg Lys Asp Phe Gly
261                                                                              320
 CTT CCC CAG GAG ATG GTG GAG GGC GAC CAG CTC CAG AAG GAC CAG GCC TTC CCT GTG CTC
 38                                                                           57
 Leu Pro Gln Glu Met Val Glu Gly Asp Gln Leu Gln Lys Asp Gln Ala Phe Pro Val Leu
321                                                                              380
 TAC GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC TAC ACA GAG CAC TCC TCT GCT GCC TGG
 58                                                                           77
 Tyr Glu Met Leu Gln Gln Ser Phe Asn Leu Phe Tyr Thr Glu His Ser Ser Ala Ala Trp
381                                                                              440
 GAC ACC ACC CTC CTG GAG CAG CTC TGC ACT GGA CTC CAA CAG CAG CTG GAC CAC CTG GAC
 78                                                                           97
 Asp Thr Thr Leu Leu Glu Gln Leu Cys Thr Gly Leu Gln Gln Gln Leu Asp His Leu Asp
441         ↓                                                                    500
 ACC TGC AGG GGT CAA GTG ATG GGA GAG GAA GAC TCT GAA CTG GGT AAC ATG GAC CCC ATT
 98                                                                          117
 Thr Cys Arg Gly Gln Val Met Gly Glu Glu Asp Ser Glu Leu Gly Asn Met Asp Pro Ile
501                                                                              560
 GTG ACC GTG AAG AAG TAC TTC CAG GGC ATC TAT GAC TAC CTG CAA GAG AAG GGA TAC AGC
 118                                                                         137
 Val Thr Val Lys Lys Tyr Phe Gln Gly Ile Tyr Asp Try Leu Gln Gln Lys Gly Tyr Ser
561                                                                              620
 GAC TGC GCC TGG GAA ATC GTC AGA GTC GAG ATG ATG AGA GCC CTC ACT GTA TCA ACC ACC
 138                                                                         157
 Asp Cys Ala Trp Glu Ile Val Arg Val Glu Met Met Arg Ala Leu Thr Val Ser Thr Thr
621                                                         666
 TTG CAA AAA AGG TTA ACA AAG ATG GGT GGA GAT CTG AAC TCA CCT TGATGACTCTTGCCGACTA
 158                                                        172
 Leu Gln Lys Arg Leu Thr Lys Met Gly Gly Asp Leu Asn Ser Pro

                                                                              764
AGATGCCACATCAGCCTCCTACACCCGCCTGTGTTCATTTCAGAAGACTCTGATTTCTGCTCCAGCCACCAAATTCATTG

                                                                              844
AATTACTTTAGCTGATACTTTGTCAGTAGTAAAAAGCAAGTAGATATAAAAGTATTCAGCTGTAGGGGCATGAGTCCTGA

                                                                              924
AATGATGCCTTCCCTGATGTTATCTGTTGCTGATTTATTTATACCTTCTAGCATTTAACATACTTAAAATATTAGGAAAT

                                              972
TTGTTAAGTTACATTTACATCTGTACATCATATTAAAATTTCTAAAACAAAAAAAAAA
```

Fig. 7



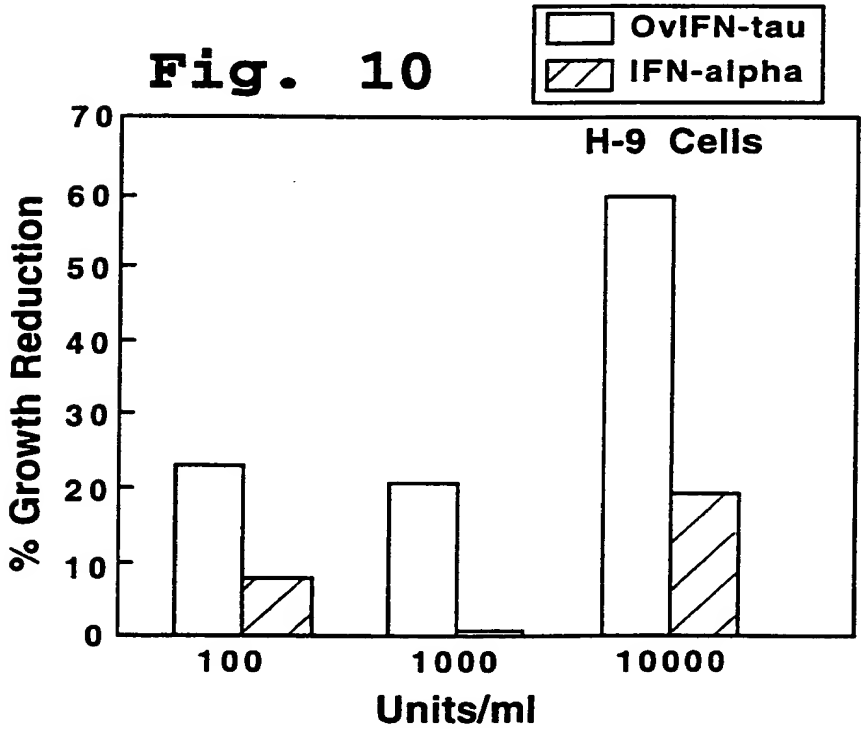


Fig. 11A

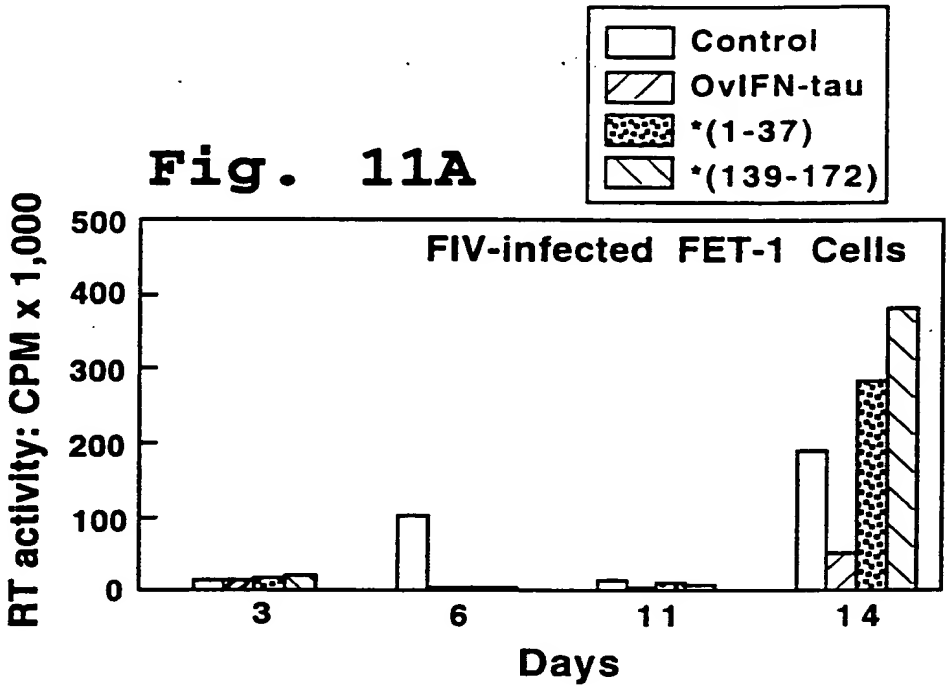


Fig. 11B

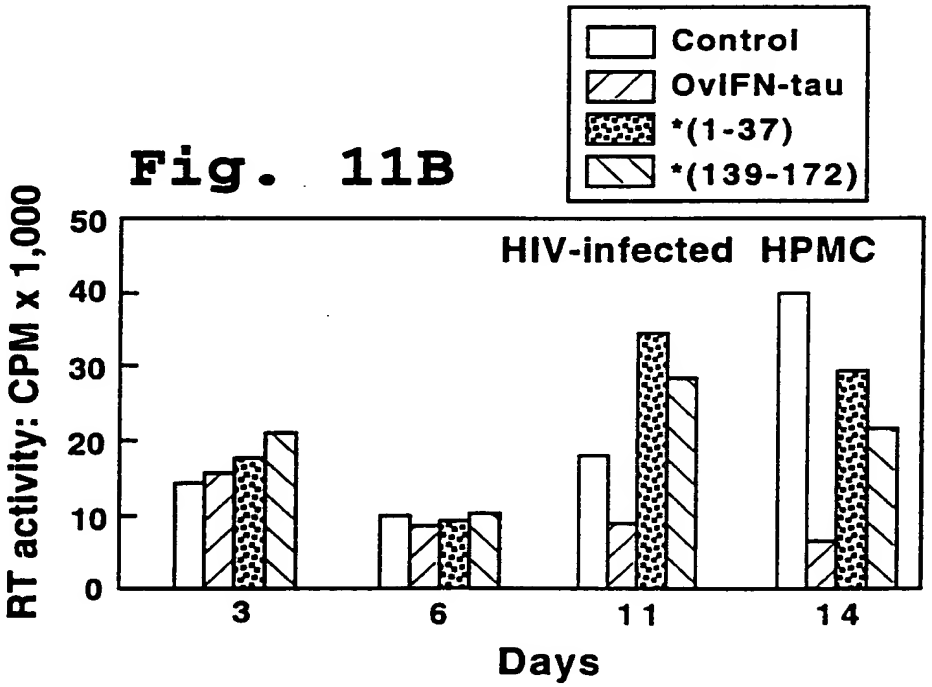


Fig. 12

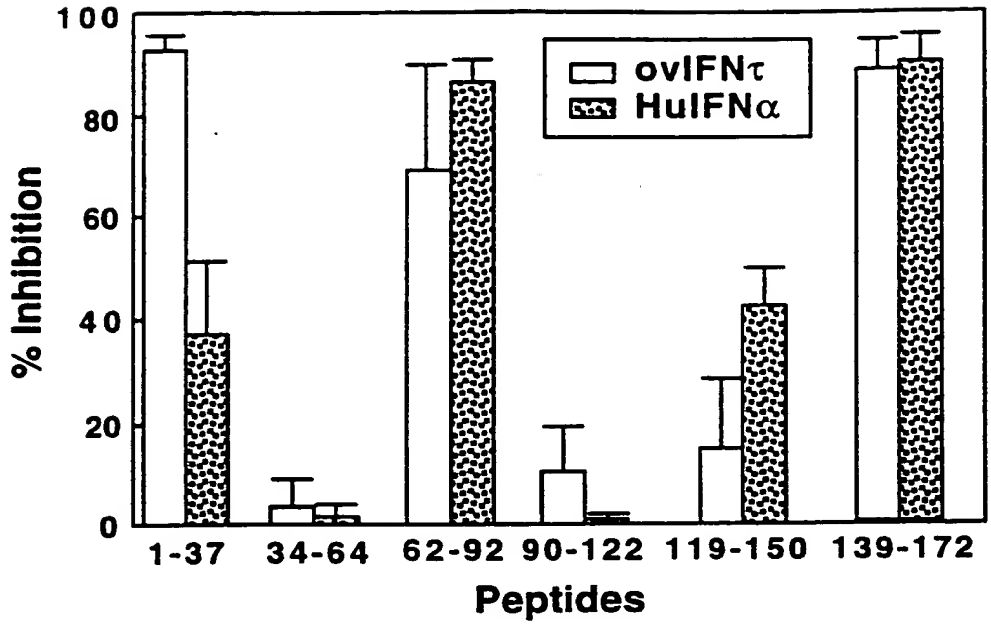


Fig. 13

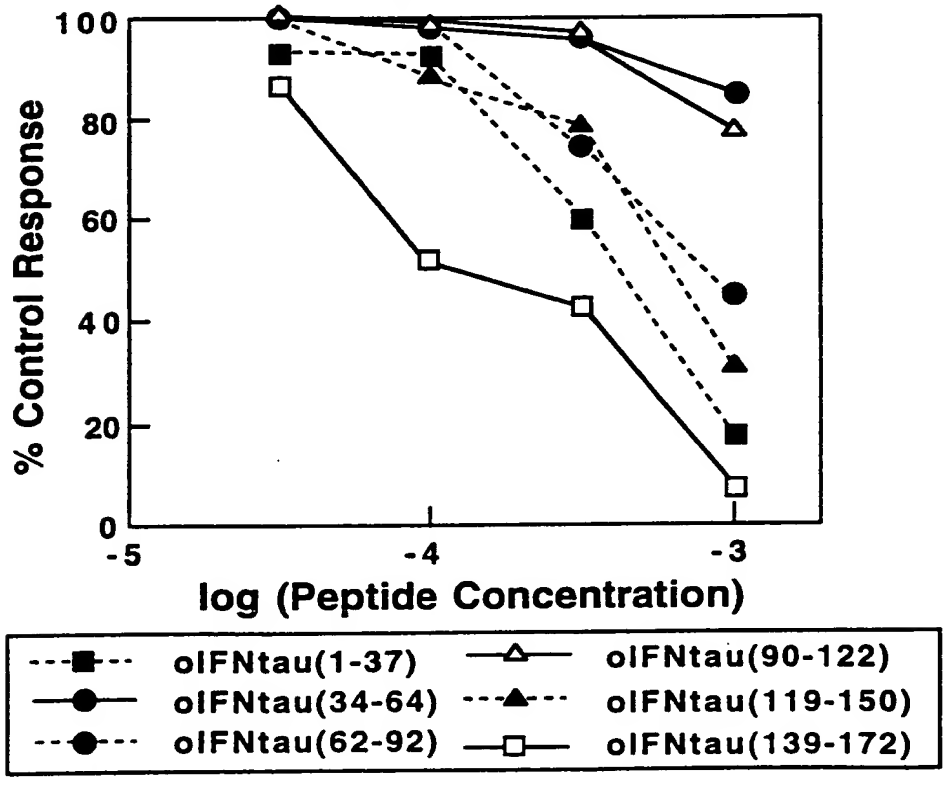
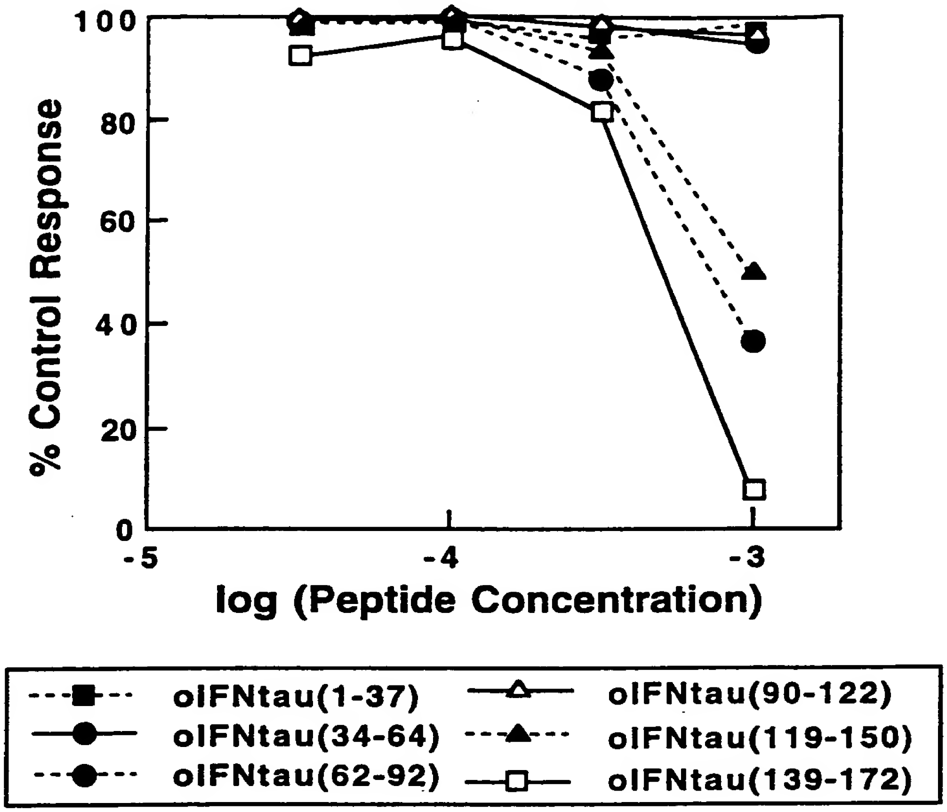


Fig. 14



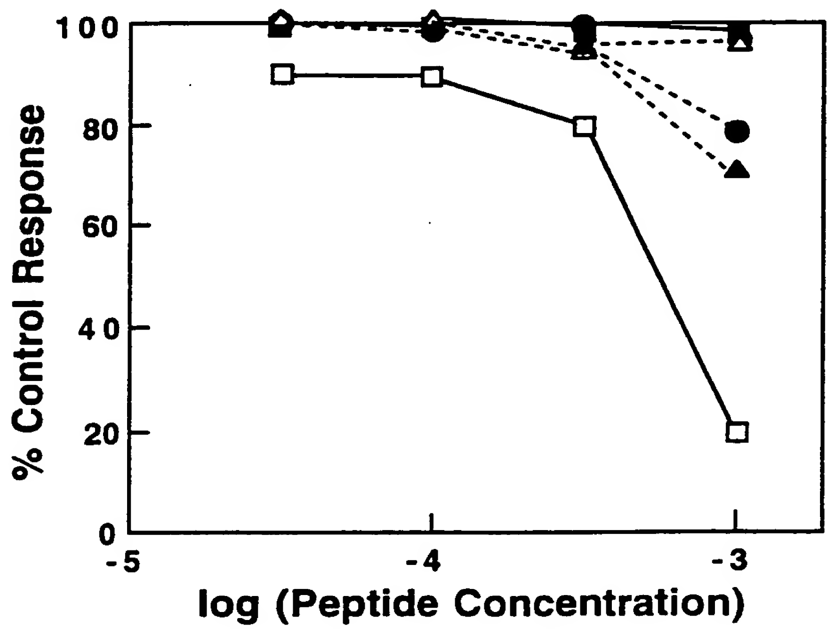


Fig. 15

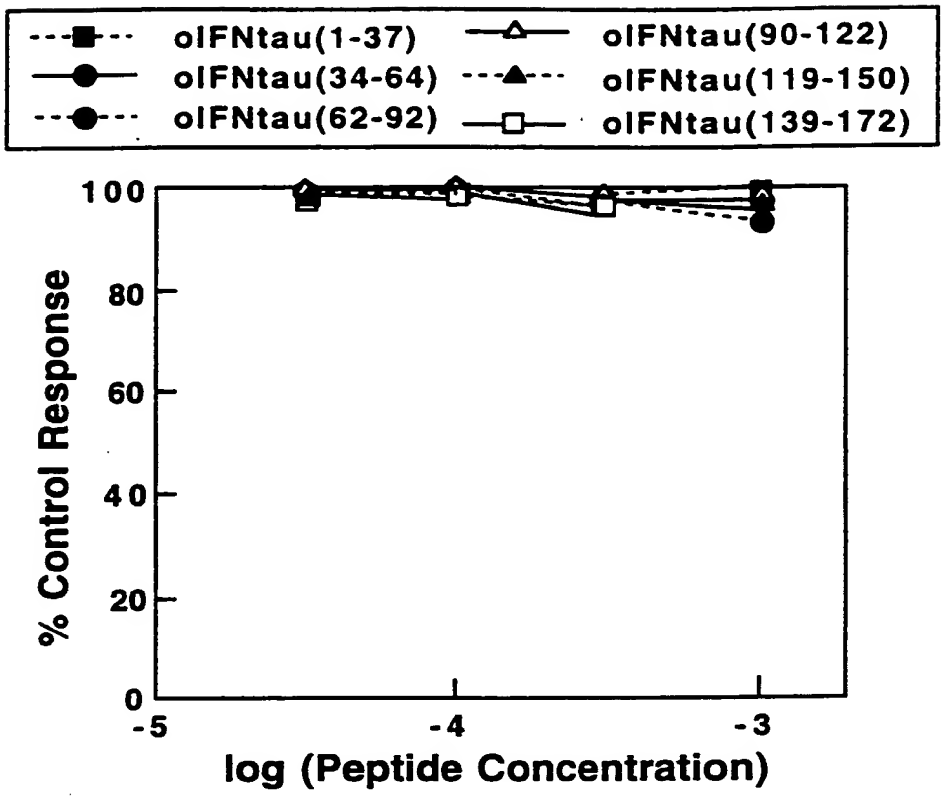


Fig. 16

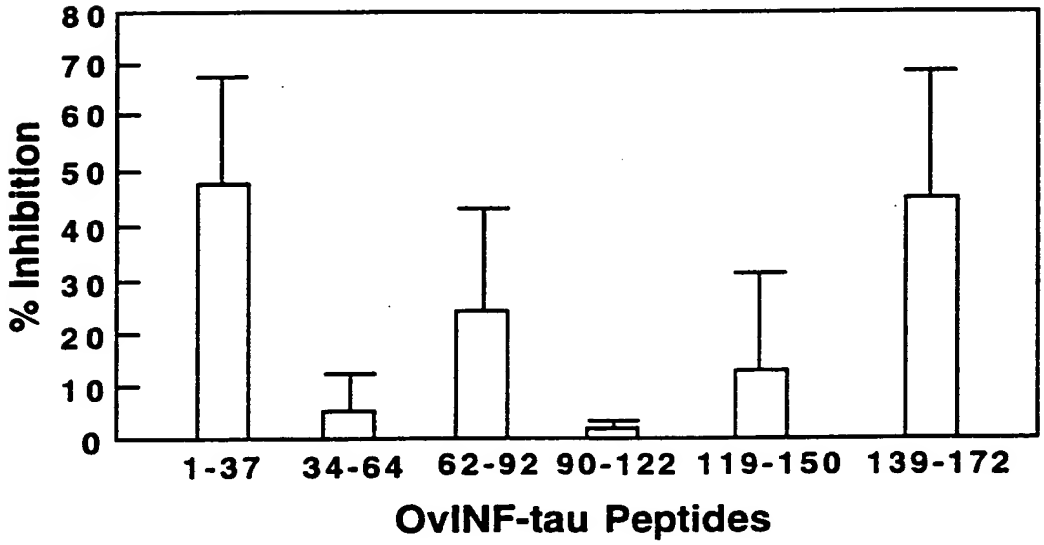


Fig. 17

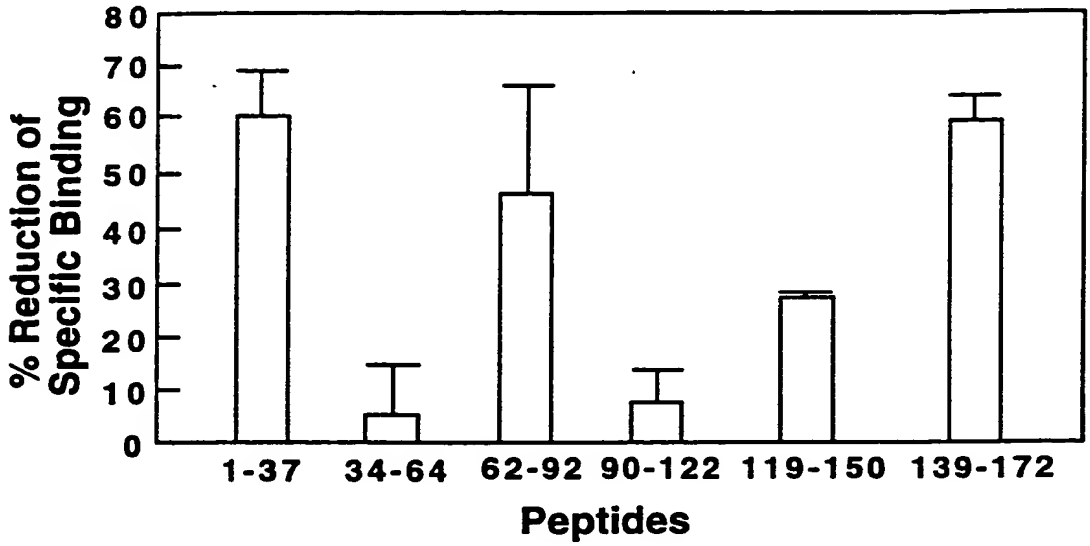


Fig. 18

```
                                  -23                                                      -9
                                  Met ala phe val leu ser leu leu met ala leu val leu val ser
oINFt                        cccc ATG GCC TTC GTG CTC TCT CTA CTG ATG GCC CTG GTG CTG GTC AGC
LEXY.5                       cccc                               c
TOSHI.9                        cc                               c
TOSHI.10                       cc                               c

                  -8                           -1  +1                                      11
                  tyr gly pro gly gly ser leu gly cys tyr leu ser arg lys leu met leu asp ala
                  TAT GGC CCA GGA GGA TCT CTG GGT TGT TAC CTA TCT CGG AAA CTC ATG CTG GAT GCC
                    c                   c             G     g       A   C   A  G        T   G
                    c                   c         (---)G    g      A    C  A  G         T   G
                    c       g           c     C G       G     g       A   C   A  G        T   G

                  12                               20                                      30
                  arg glu asn leu lys leu leu asp arg met asn arg leu ser pro his ser cys leu
                  AGG GAG AAC CTC AAG CTC CTG GAC CGA ATG AAC AGA CTC TCC CCT CAT TCC TGT CTG
                      A            G              GA       GG                  GC   TT
                      A            G               A       GG                  GC   TT
                    C C            G           G   A       GG              T   GC  T

                  31                                   40                                  49
                  gln asp arg lys asp phe gly leu pro gln glu met val glu gly asp gln leu gln
                  CAG GAC AGA AAA GAC TTT GGT CTT CCC CAG GAG ATG GTG GAG GGC GAC CAG CTC CAG
                                        c  C  t  a           a                  G
                                        c  C   t a     TAG   a                   G
                                        c  C  t  a                           t  G
Clone 21                                          !                          t  G
Clone 35                                          !                          t  G
Clone 15                                          !                             G
Clone 18                                          !                        T  AG      T

                  50                                       60                              68
                  lys asp gln ala phe pro val leu tyr glu met leu gln gln ser phe asn leu phe
                  AAG GAC CAG GCC TTC CCT GTG CTC TAC GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC
                  G    C          A   T           C T
                  G    C          A   T           C T
                  G    C          A   T           C
                  G    C          A   T           C
                  G    C          A   T           C
                  G    C          A   T           C   A
                  G    C          A T T           C T

                  69                                           80                          87
                  tyr thr glu his ser ser ala ala try asp thr thr leu leu glu gln leu cys thr
                  TAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC CTC CTG GAG CAG CTC TGC ACT
                  C                                                                   C
                  C                                                                   C
                  C                                                                   C
                  C                                                                   C
                  C                                                                   C
                  C            G                                                      C
                  C    A       G                            t                         CT
```

Fig. 19A

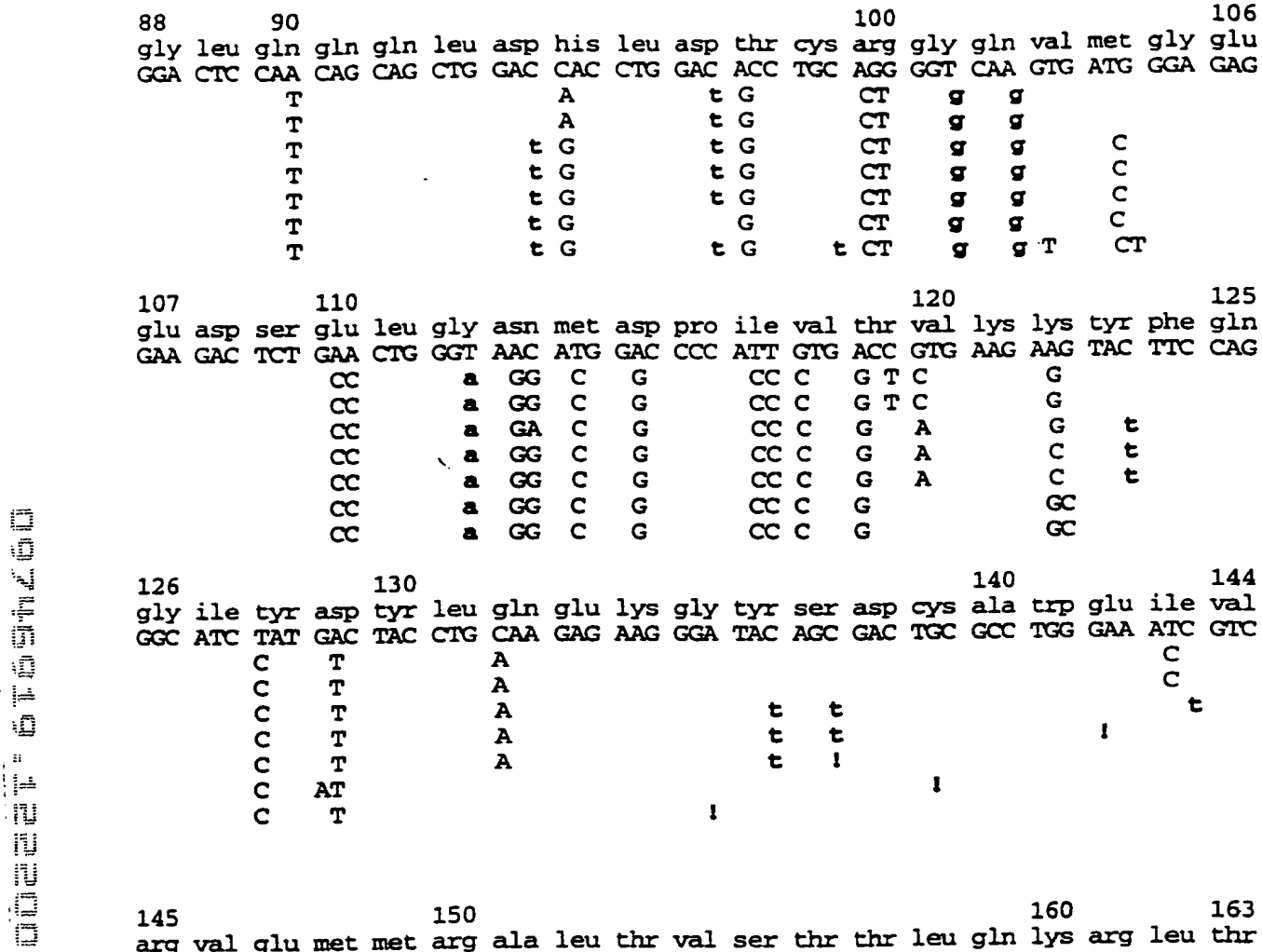


Fig. 19B

```
                -23                                                    -9
oTP-1           Met ala phe val leu ser leu leu met ala leu val leu val ser
LEXY.5
TOSHI.9
TOSHI.10

-8                              -1  +1                                  11
tyr gly pro gly gly ser leu gly cys tyr leu ser arg lys leu met leu asp ala
                                    asp         gln asn his val     val gly
                                (---)asp         gln asn his val     val gly
                              arg   asp         gln asn his val     val gly

12                                  20                                  30
arg glu asn leu lys leu leu asp arg met asn arg leu ser pro his ser cys leu
    lys         arg             glu     arg                 arg phe
    lys         arg             gln     arg                 arg phe
ser gln         arg         gly gln     arg             leu arg phe

31                                  40                                  49
gln asp arg lys asp phe gly leu pro gln glu met val glu gly asp gln leu gln
                        ala                                 gly
                        ala         (Stop)                   gly
                        ala                                 gly
Clone 21                            !                           gly
Clone 35                          !                         gly
Clone 15                          !                         gly
Clone 18                          !                     val ser     phe

50                                      60                          68
lys asp gln ala phe pro val leu tyr glu met leu gln gln ser phe asn leu phe
glu ala         ile ser         his
glu ala         ile ser         his
glu ala         ile ser         his
glu ala         ile ser         his
glu ala         ile ser         his
glu ala         ile ser         his lys
glu ala         ile ser         his

69                                          80                      87
tyr thr glu his ser ser ala ala try asp thr thr leu leu glu gln leu cys thr
his                                                             arg
his                                                             arg
his                                                             arg
his                                                             arg
his                                                             arg
his         arg                                                 arg
his lys     arg                                                 leu
```

Fig. 20A

88		90									100					106
gly	leu	gln	gln	gln	leu	asp	his	leu	asp	thr	cys	arg	gly	gln	val	met	gly	glu
		his					asn			ala		leu						
		his					asn			ala		leu						
		his					asp			ala		leu				thr		
		his					asp			ala		leu				thr		
		his					asp			ala		leu				thr		
		his					asp			ala		leu				thr		
		his					asp			ala		leu			leu	thr		

107			110									120					125
glu	asp	ser	glu	leu	gly	asn	met	asp	pro	ile	val	thr	val	lys	lys	tyr	phe	gln
			ala			arg	thr	gly		thr	leu	ala	leu		arg			
			ala			arg	thr	gly		thr	leu	ala	leu		arg			
			ala			arg	thr	gly		thr	leu	ala	met		arg			
			ala			arg	thr	gly		thr	leu	ala	met		thr			
			ala			arg	thr	gly		thr	leu	ala	met		thr			
			ala			arg	thr	gly		thr	leu	ala			ser			
			ala			arg	thr	gly		thr	leu	ala			ser			

126				130										140				144
gly	ile	tyr	asp	tyr	leu	gln	glu	lys	gly	tyr	ser	asp	cys	ala	trp	glu	ile	val
		his	val			lys											thr	
		his	val			lys											thr	
		his	val			lys										!		
		his	val			lys												
		his	val			lys						!						
		his	ile										!					
		his	val							!								

145					150										160			163
arg	val	glu	met	met	arg	ala	leu	thr	val	ser	thr	thr	leu	gln	lys	arg	leu	thr
	leu		ile			ser	phe	ser	ser	leu	ile	ser			glu			arg
			ile			ser	phe	ser	ser	leu	ile	ser			glu			arg
	leu		ile			ser		ser	ser			ser		his				arg

164							172	
lys	met	gly	gly	asp	leu	asn	ser	pro	**stop**
met		asp				ser			**stop**
met		asp				ser			**stop**
met		asp				ser			**stop**

Fig. 20B

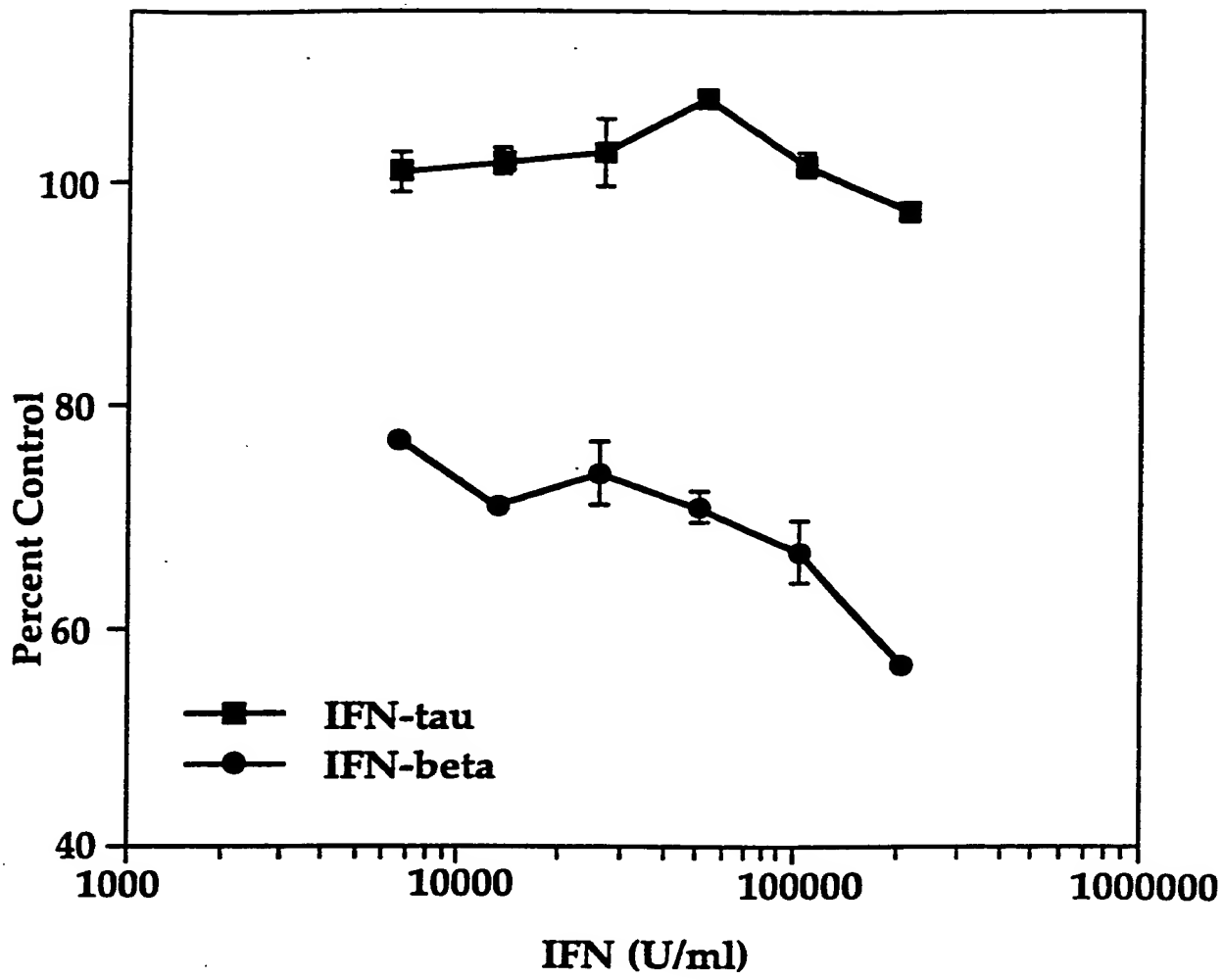


Fig. 21